

1627

BIOTECHNOLOGY
SYSTEMS
BRANCH

TECH CENTER 1600/2900

OCT 05 2001

RECEIVED

**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/374 338 B

Source: OIPE

Date Processed by STIC: 08/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/374 338 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ✓ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/374,338B

TIME: 13:24:31

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I374338B.raw

3 <110> APPLICANT: Heller, Michael J.
4 Windhab, Norbert
5 Anderson, Richard R.
6 Ackley, Donald E.
7 Nova, Tina S.
8 Hoppe, Hans-Ullrich
9 Hamon, Christian
11 <120> TITLE OF INVENTION: MICROELECTRONIC MOLECULAR DESCRIPTOR ARRAY DEVICES, METHODS,
PROCEDURES,
12 AND FORMATS FOR COMBINATORIAL SELECTION OF INTERMOLECULAR LIGAND BINDING
13 STRUCTURES AND FOR DRUG SCREENING
15 <130> FILE REFERENCE: Patrick Eagleman: Nanogen 241/172
17 <140> CURRENT APPLICATION NUMBER: 09/374,338B
18 <141> CURRENT FILING DATE: 1999-08-13
20 <160> NUMBER OF SEQ ID NOS: 31
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 7
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence ✓
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Synthetic test construct ✓
32 <220> FEATURE:
33 <221> NAME/KEY: modified_base
34 <222> LOCATION: (1)..(7)
35 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
38 <220> FEATURE:
39 <221> NAME/KEY: modified_base
40 <222> LOCATION: (1)..(1)
41 <223> OTHER INFORMATION: Base 1 is tryptamine
44 <220> FEATURE:
45 <221> NAME/KEY: modified_base
46 <222> LOCATION: (7)..(7)
47 <223> OTHER INFORMATION: Base 7 is modified with Texas Red
50 <400> SEQUENCE: 1
W--> 51 ngaaggg
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 14
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic test construct
62 <220> FEATURE:
63 <221> NAME/KEY: modified_base
64 <222> LOCATION: (1)..(14)
65 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
68 <220> FEATURE:
69 <221> NAME/KEY: modified_base

Does Not Comply
Corrected Diskette Needed

n can only represent a
single nucleotide base at any
single location.

FYI - tryptamine is an
amino acid or protein

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/374,338B

TIME: 13:24:31

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I374338B.raw

70 <222> LOCATION: (1)..(1)
 71 <223> OTHER INFORMATION: Base 1 is modified with Biotin
 74 <220> FEATURE:
 75 <221> NAME/KEY: modified_base
 76 <222> LOCATION: (8)..(8)
 77 <223> OTHER INFORMATION: Base 8 is tryptamine
 80 <400> SEQUENCE: 2
 W--> 81 cccttcttcc cccg
 84 <210> SEQ ID NO: 3
 85 <211> LENGTH: 7
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: Synthetic test construct
 93 <220> FEATURE:
 94 <221> NAME/KEY: modified_base
 95 <222> LOCATION: (1)..(7)
 96 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
 99 <220> FEATURE:
 100 <221> NAME/KEY: modified_base
 101 <222> LOCATION: (1)..(1)
 102 <223> OTHER INFORMATION: Base 1 is modified with Cyanine-3 flourescent dye
 105 <220> FEATURE:
 106 <221> NAME/KEY: modified_base
 107 <222> LOCATION: (7)..(7)
 108 <223> OTHER INFORMATION: Base 7 is tryptamine
 111 <400> SEQUENCE: 3
 W--> 112 cggggg Error
 115 <210> SEQ ID NO: 4
 116 <211> LENGTH: 7
 117 <212> TYPE: DNA
 118 <213> ORGANISM: Artificial Sequence
 120 <220> FEATURE:
 121 <223> OTHER INFORMATION: Synthetic test construct
 124 <220> FEATURE:
 125 <221> NAME/KEY: modified_base
 126 <222> LOCATION: (1)..(7)
 127 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
 130 <220> FEATURE:
 131 <221> NAME/KEY: modified_base
 132 <222> LOCATION: (3)..(3)
 133 <223> OTHER INFORMATION: Base 3 is tryptamine
 136 <220> FEATURE:
 137 <221> NAME/KEY: modified_base
 138 <222> LOCATION: (4)..(4)
 139 <223> OTHER INFORMATION: Base 4 is tryptamine
 142 <220> FEATURE:
 143 <221> NAME/KEY: modified_base
 144 <222> LOCATION: (5)..(5)

n can only represent a
 single nucleotide base at
 any single location.

n can only represent a
 single nucleotide base at
 any single location
 FYI tryptamine is an
 amino acid

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/374,338B

TIME: 13:24:31

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I374338B.raw

145 <223> OTHER INFORMATION: Base 5 is tryptamine
 148 <400> SEQUENCE: 4
 W--> 149 ccnnngg 7
 152 <210> SEQ ID NO: 5
 153 <211> LENGTH: 7
 154 <212> TYPE: DNA
 155 <213> ORGANISM: Artificial Sequence
 157 <220> FEATURE:
 158 <223> OTHER INFORMATION: Synthetic test construct
 161 <220> FEATURE:
 162 <221> NAME/KEY: modified_base
 163 <222> LOCATION: (1)..(7)
 164 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
 167 <220> FEATURE:
 168 <221> NAME/KEY: modified_base
 169 <222> LOCATION: (1)..(1)
 170 <223> OTHER INFORMATION: Base 1 modified with Fluorophore
 173 <220> FEATURE:
 174 <221> NAME/KEY: modified_base
 175 <222> LOCATION: (7)..(7)
 176 <223> OTHER INFORMATION: Base 7 modified with a Peptide
 179 <220> FEATURE:
 180 <221> NAME/KEY: modified_base
 181 <222> LOCATION: (7)..(7) *Errored*
 182 <223> OTHER INFORMATION: Base 7 is tryptamine
 185 <400> SEQUENCE: 5
 W--> 186 cgggggg 7
 189 <210> SEQ ID NO: 6
 190 <211> LENGTH: 8
 191 <212> TYPE: DNA
 192 <213> ORGANISM: Artificial Sequence
 194 <220> FEATURE:
 195 <223> OTHER INFORMATION: Synthetic test construct
 198 <220> FEATURE:
 199 <221> NAME/KEY: modified_base
 200 <222> LOCATION: (1)..(8)
 201 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
 204 <220> FEATURE:
 205 <221> NAME/KEY: modified_base
 206 <222> LOCATION: (1)..(1)
 207 <223> OTHER INFORMATION: Base 1 modified with a Peptide
 210 <220> FEATURE:
 211 <221> NAME/KEY: modified_base
 212 <222> LOCATION: (1)..(1) *Errored*
 213 <223> OTHER INFORMATION: Base 1 is tryptamine
 216 <220> FEATURE:
 217 <221> NAME/KEY: modified_base
 218 <222> LOCATION: (8)..(8)
 219 <223> OTHER INFORMATION: Base 8 is any nucleotide *OK*

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/374,338B

TIME: 13:24:31

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I374338B.raw

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222 <400> SEQUENCE: 6
W--> 223 ngaagggn 8
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 14
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Synthetic test construct
235 <220> FEATURE:
236 <221> NAME/KEY: modified_base
237 <222> LOCATION: (1)..(14)
238 <223> OTHER INFORMATION: Entire sequence is Pyranosyl RNA
241 <220> FEATURE:
242 <221> NAME/KEY: modified_base
243 <222> LOCATION: (1)..(1)
244 <223> OTHER INFORMATION: Base 1 modified with Biotin
247 <220> FEATURE:
248 <221> NAME/KEY: modified_base
249 <222> LOCATION: (7)..(7)
250 <223> OTHER INFORMATION: Base 7 is tryptamine
253 <220> FEATURE:
254 <221> NAME/KEY: modified_base
255 <222> LOCATION: (7)..(8)
256 <223> OTHER INFORMATION: Bases 7 and 8 are modified by Peptide connection.
259 <400> SEQUENCE: 7
W--> 260 cccttctc cccg 14
263 <210> SEQ ID NO: 8
264 <211> LENGTH: 6
265 <212> TYPE: PRT
266 <213> ORGANISM: Artificial Sequence ✓
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Synthetic test construct ✓
272 <220> FEATURE:
273 <221> NAME/KEY: PEPTIDE
274 <222> LOCATION: (1)..(1)
275 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
278 <400> SEQUENCE: 8
280 Cys Leu Ser Leu Glu Gly
281 1 5
283 <210> SEQ ID NO: 9
284 <211> LENGTH: 6
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial Sequence ✓
288 <220> FEATURE: ✓
-----
289 <223> OTHER INFORMATION: Synthetic test construct
292 <220> FEATURE:
293 <221> NAME/KEY: PEPTIDE
294 <222> LOCATION: (1)..(1)
295 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA

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RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/374,338B

TIME: 13:24:31

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I374338B.raw

298 <400> SEQUENCE: 9
300 Cys Ser Leu Glu Ser Gly
301 1 5
303 <210> SEQ ID NO: 10
304 <211> LENGTH: 6
305 <212> TYPE: PRT
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic test construct ✓
312 <220> FEATURE:
313 <221> NAME/KEY: PEPTIDE
314 <222> LOCATION: (1)..(1)
315 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
318 <400> SEQUENCE: 10
320 Cys Leu Leu Ser Glu Gly
321 1 5
323 <210> SEQ ID NO: 11
324 <211> LENGTH: 6
325 <212> TYPE: PRT
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Synthetic test construct ✓
332 <220> FEATURE:
333 <221> NAME/KEY: PEPTIDE
334 <222> LOCATION: (1)..(1)
335 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
338 <400> SEQUENCE: 11
340 Cys Ser Arg Ser Arg Gly
341 1 5
343 <210> SEQ ID NO: 12
344 <211> LENGTH: 6
345 <212> TYPE: PRT
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Synthetic test construct
352 <220> FEATURE:
353 <221> NAME/KEY: PEPTIDE
354 <222> LOCATION: (1)..(1)
355 <223> OTHER INFORMATION: 1st amino acid is modified with pyranosyl RNA
358 <400> SEQUENCE: 12
360 Cys Ser Arg His Arg Gly
361 1 5
363 <210> SEQ ID NO: 13
364 <211> LENGTH: 6
365 <212> TYPE: PRT
366 <213> ORGANISM: Artificial Sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: Synthetic test construct
372 <220> FEATURE:

VERIFICATION SUMMARY

DATE: 08/23/2001

PATENT APPLICATION: US/09/374,338B

TIME: 13:24:32

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I374338B.raw

L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31